

Sequence alignment of various TGFBR genes from different species. The alignment shows conservation of amino acid residues across the protein. A color scale at the top indicates hydrophilicity (red for hydrophobic, green for hydrophilic). The alignment spans from position 10 to 190, 210 to 390, 410 to 590, and 610 to 790. A vertical bar on the left indicates the start of each sequence.

Sequence alignment of various TGFBR isoforms from different species. The alignment shows conservation of amino acid residues across the protein sequence. The top row shows positions 1-990, and the bottom row shows positions 1410-1590. Colored bars indicate hydrophilicity (red), hydrophobicity (blue), and polar uncharged (green).

....|..

6981000.m  
38085380.m  
27806993.m  
HSER.h  
27806997.m  
CYGF.h  
38086777.m  
16758684.m  
6680135.m  
13242283.m  
27806995.m  
CYGD.h  
18543337.m  
31198009.i  
24644018.f **AEQILLSR**  
lias\_TGFBR